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Subject: Two new papers on outbreak in Wuhan

Attachments: Yue et al. 2017.pdf; Amenola et al. 2021.pdf; Bloom 2021.pdf; 2022.02.26_worobey_preprint.pdf; Pekar_Zoonosis.pdf

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Hello All,

Was just going over two papers that came out on the Wuhan outbreak (Pekar and Worobey attached) and wanted to share some thoughts/ideas.

First of all, it seems that the two hypotheses being posited around the outbreak are that either (1) the virus jumped from a non-human host to humans and spread rapidly, or (2) the virus was manufactured in WIV using CRISPR or other high level technology and released on purpose. We should also consider other options such as

(3) the virus appeared in a non-human host (e.g. mink farms in northern China) and WIV collected samples from there, brought them back to Wuhan to study and the virus was accidentally released.

From the link below –

“A little known fact is that in 2019 Shandong produced 6.5 million mink pelts, down from nearly 15 million in 2018...production of hides from foxes (5,7 million) and racoon dogs (3 million) remained perfectly stable”

<https://reporterre.net/Mounting-evidence-suggests-mink-farms-in-China-could-be-the-cradle-of-Covid-19-22020>

In further support of hypothesis (3) – given how rapidly this thing spread through mink populations everywhere else in the world (Denmark, Netherlands, Utah, Michigan, Norway, Russia...), it would be amazing if the farms in China were *unaffected*. And the mortality is so high in these hosts that it certainly would have triggered an investigation. It also offers a potential movement of the virus across the globe – not through mink per se, but rather through mink *trade* including machines to de-pelt the animals made in Demark, wholesalers, etc. The Silk Road was how the Black Death spread for example – see Yue et al. attached. Digging into the mink trade a bit might be useful.

The Worobey et al. paper focuses on looking at the spatial distribution of the first cases to test the hypothesis that the virus came from the live animal market in Wuhan, which they claim is definitive evidence that hypothesis 1 is correct and hypothesis 2 is therefore false.

Comments and criticisms:

They definitely show that the cases clustered around the live market. However, in Figure 1E they show a kernel density map of cases using cel phone data from Weibo – they mark the live animal market but not the Wuhan Institute of Virology. I put a comment there in the attached PDF. **One of their density clusters sits on WIV, about 10km away and the densest cluster sits half way between WIV and the market.** Therefore, if they had tested the hypothesis that the cases were centered around WIV and not the market, the test likely would have been significant.

Their unexpected finding that lineages A and B are both associated with the live animal market is interesting – my haplotype network shows that Lineage A **was derived via a recombination event in Wuhan – which is consistent with movement among human and non-human hosts within the live animal market. Mink were sold in that market at that time (Table 2). I attached the haplotype network.**

We know that sequences were deleted from NCBI by China that are rooted further back from the Wuhan sequence (Bloom 2021 attached). So we know we are only “looking under the lamplight” and not including previous data.

They authors also do not address the fact that the SARS-CoV-2 Spike sequence was identified in a child with Kawasaki Disease in Rome, Italy in early December 2019, 3 months before it broke there in Lombardy
(Amendola et al. attached).

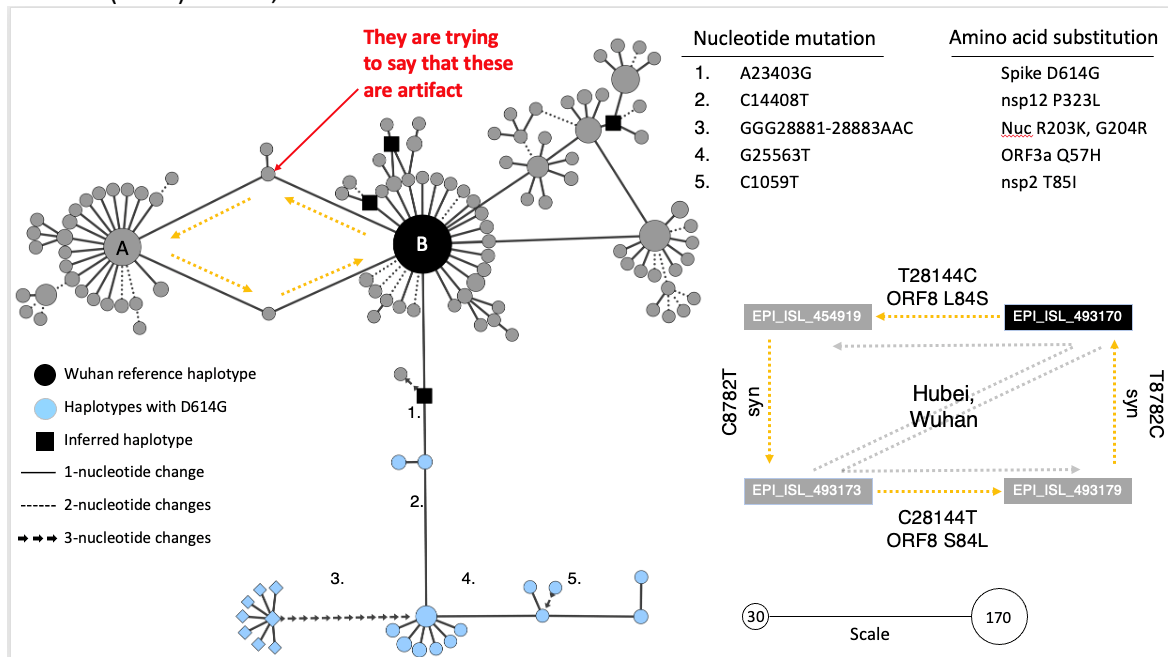
Finally – the second paper (Pekar et al) is a deeper dive into the molecular evolution and quite frankly is a bit shaky. I’m still trying to work out how they “filtered” their data – the sequences I used to detect recombination are definitely in their sampled data. In the text they describe several crappy sequences that they use to explain why they threw out most of the sequences that show a potential recombination (homoplasy). From what I can tell they “explain” away the rest of the sequences by saying it was “convergent evolution” (at a synonymous site no less).

I’m still working on the recombination stuff and will update when that is done but I think this virus was recombining from the start and part of that involved looping through non-human hosts.

Cheers

Mike

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